TRUNCATED BOOLEAN MATRICES FOR DNA COMPUTATION

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ABSTRACT

Although DNA computing has emerged as a new computing paradigm with its massive parallel computing capabilities, the large number of DNA required for larger size of computational problems still remain as a stumbling block to its development as practical computing. In this paper, we propose a modification to implement a physical experimentation of two Boolean matrices multiplication problem with DNA computing. The Truncated Matrices reduces the number of DNA sequences and lengths utilized to compute the problem with DNA computing.

KEYWORDS

DNA computation, Boolean Matrices, Bio-molecular tools, Parallel Overlap Assembly

1. INTRODUCTION

When Leonard M Adleman first proposed the use of DNA for computation in solving the Hamiltonian Path Problem (HPP) in 1994, the computation was implemented in an in-vitro experimentation with designed DNA oligonucleotide sequences to represent the vertices and the edges. The solution to the computation was then derived from the chemical reactions via bio-molecular tools such as hybridication-ligation method, polymerase chain reaction and cutting by restriction enzymes. The output was then visualized in gel electrophoresis process. The computation of seven-node HPP took seven days to complete [1]. Since then, many proposals were presented to compute problems with DNA computation but most of them still rely on the L.M Adleman's architecture to carry out the computation. Although the massive parallel computing capabilities of DNA computing promises faster and denser computation there remain several drawbacks which prevent it from becoming a practical computing material. One reason is the exponential requirement of DNA in computing larger size of computational problem [2].

Current strategy in DNA computing is to embed the computation problems in the DNA oligonucleotides sequences and derive the solution by eliminating incorrect DNA via selective processes. For a seven-node HPP, the problem was encoded in a 20 oligonucleotide sequence. For a 23-node HPP, the computation will require 1 kg of DNA and for a 70-node HPP, the computation will require 10^{25} kg of DNA to represent all the nodes [3]. Other problems such as maximal clique problems, vertex-cover problems and set packaging problems all show similarly exponential requirement of DNA and increased time for the computations. LaBean et al (2000) proposed that an1.89^n volume, O (n^2+m^2) time molecular algorithm for the 3-coloring problem

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